

SEQUENCE LISTING

<110> Barber, Elizabeth K

<120> Gene Expression Control Element DNA

<130> 896034605001

<150> US 60/237,079

<151> 2000-09-30

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 137

<212> DNA

<213> human

<220>

<221> exon

<222> (3) .. (137)

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<221> polyA_site

<222> (130) .. (135)

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0996264-092801

<400> 1
 at tat aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg 47
 Tyr Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu
 1 5 10
 tga act cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga 95
 Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys
 15 20 25
 ggt aga aat agc atg aga agc cgt gtt tga tgt taa tta att 137
 Gly Arg Asn Ser Met Arg Ser Arg Val Cys Leu Ile
 30 35 40

<210> 2

<211> 996

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<222> (1)..(996)

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<221> misc_feature

<222> (710)..(996)

<223> Nucleotides 710-996 are homologous to a portion of human dystroph
 in DNA in the region of exon 79 except that nucleotides 860-996 a
 re inverted in comparison to the orientation of the same sequence
 in the dystrophin DNA

<400> 2
 gtg gtt tga ttg ata gta aaa aaa atg ttc gtt aat aca agt aga gag 48
 Val Val Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu
 1 5 10 15

taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc 96
 Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro

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atc	atg	gaa	tat	tcc	tgt	tct	gat	aga	aat	ctt	gtg	ctt	atc	tat	gga	144																		
Ile	Met	Glu	Tyr	Ser	Cys	Ser	Asp	Arg	Asn	Leu	Val	Leu	Ile	Tyr	Gly																			
				35					40					45																				
att	ctt	ttg	ata	tat	att	tac	att	ggg	aac	ctg	aat	gta	gct	tga	cat	192																		
Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	Gly	Asn	Leu	Asn	Val	Ala		His																			
				50					55					60																				
ttt	tcc	atg	taa	aca	cca	gta	gcc	tga	tcc	aac	att	aag	ctg	ata	cta	240																		
Phe	Ser	Met		Thr	Pro	Val	Ala		Ser	Asn	Ile	Lys	Leu	Ile	Leu																			
				65					70					75																				
aca	aac	aac	gtg	taa	tgg	ctt	cat	taa	taa	ggc	ttt	gct	tct	tcc	tgg	288																		
Thr	Asn	Asn	Val		Trp	Leu	His			Gly	Phe	Ala	Ser	Ser	Trp																			
				80					85																									
aaa	ctg	gtg	aaa	aat	caa	acc	ttg	ttg	tgt	aca	ccc	tcg	atg	cag	ctt	336																		
Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu	Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu																			
				90					95					100																				
ctg	tgt	tgt	ctt	cac	cca	gaa	atg	ggg	aat	gat	ttc	cca	aat	ggc	aaa	384																		
Leu	Cys	Cys	Leu	His	Pro	Glu	Met	Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys																			
				105					110					115					120															
gaa	aca	gag	tga	tgc	tat	cta	tct	gca	cct	ttt	gta	aag	tct	gtc	ttt	432																		
Glu	Thr	Glu		Cys	Tyr	Leu	Ser	Ala	Pro	Phe	Val	Lys	Ser	Val	Phe																			
				125					130					135																				
ctt	tct	ctt	tgt	ttt	cca	gga	cac	aat	gta	gga	agt	ctt	ttc	cac	atg	480																		
Leu	Ser	Leu	Cys	Phe	Pro	Gly	His	Asn	Val	Gly	Ser	Leu	Phe	His	Met																			
				140					145					150																				
gca	gat	gat	ttg	ggc	aga	gcg	atg	gag	tcc	tta	gta	tca	gtc	atg	aca	528																		
Ala	Asp	Asp	Leu	Gly	Arg	Ala	Met	Glu	Ser	Leu	Val	Ser	Val	Met	Thr																			
				155					160					165																				
gat	gaa	gaa	gga	gca	gaa	taa	atg	ttt	tac	aac	tcc	tga	ttc	ccg	cat	576																		
Asp	Glu	Glu	Gly	Ala	Glu		Met	Phe	Tyr	Asn	Ser		Phe	Pro	His																			
				170					175					180																				
ggg	ttt	tat	aat	att	cat	aca	aca	aag	agg	att	aga	cag	taa	gag	ttt	624																		
Gly	Phe	Tyr	Asn	Ile	His	Thr	Thr	Lys	Arg	Ile	Arg	Gln		Glu	Phe																			
				185					190					195																				
aca	aga	aat	aaa	tct	ata	ttt	ttg	tga	agg	gta	gtg	gta	tta	tac	tgt	672																		
Thr	Arg	Asn	Lys	Ser	Ile	Phe	Leu		Arg	Val	Val	Val	Leu	Tyr	Cys																			
				200					205					210																				
aga	ttt	cag	tag	ttt	cta	agt	ctg	tta	ttg	ttt	tgt	taa	caa	tgg	cag	720																		
Arg	Phe	Gln		Phe	Leu	Ser	Leu	Leu	Leu	Phe	Cys		Gln	Trp	Gln																			

tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816
 Cys Lys Ile Leu Ile Ala Lys Leu Ala Ile Ser Leu Tyr Gly Thr
 245 250 255

cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 864
 His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr
 260 265 270

aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912
 Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr
 275 280

cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960
 Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg
 285 290 295

aat agc atg aga agc cgt gtt tga tgt taa tta att 996
 Asn Ser Met Arg Ser Arg Val Cys Leu Ile
 300 305

<210> 3

<211> 13

<212> PRT

<213> human

<400> 3

Met Tyr Pro Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn
 1 5 10

<210> 4

<211> 13

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<400> 4

Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala Asp Thr Met
 1 5 10

<210> 5

09066264-0906601

<211> 18
<212> PRT
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<400> 5

Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp
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Glu Glu

<210> 6
<211> 10
<212> DNA
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<400> 6
acttacctgt 10

<210> 7
<211> 22
<212> DNA
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<400> 7
ttataaagaa agaattataa ag 22

<210> 8
<211> 42
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<400> 8

09966264-092801

ccttggctat gattgattga ttgattactt actctctact tg

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<210> 9

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<212> DNA

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<210> 10

<211> 21

<212> DNA

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21

<210> 11

<211> 20

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<211> 22

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0906264-092601

<210> 13
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 <223> histone methylation site

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 <223> histone methylation site

<400> 14
 Arg Lys Asn Tyr Lys Gly Lys Arg Lys
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09966264-092801
108260-4929660

<212> DNA

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18

<210> 16

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ccagtagcct gatccaac

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ggcttcatta ataag

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ggcaaagaaa cagagtg

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<400> 20
caggacacaa tgtagga

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gttataaaga aagaattata aag

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<211> 16

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<400> 26
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<210> 27

<211> 19

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<212> DNA

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18

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22

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Met Phe Val Asn Thr Thr Lys Val Glu Lys Met Tyr Pro Ile Met Glu
1 5 10 15

Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly Ile Leu Leu
20 25 30

Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Met Lys Lys Glu Gln Asn Lys
35 40 45

Cys Phe Thr Thr Pro Asp Ser Arg Met Val Phe Ile Ile Phe Ile Gln
50 55 60

Gln Arg Gly Leu Asp Ser Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe
65 70 75 80

Cys Glu Gly Phe Tyr Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg
85 90 95

Lys Leu His Lys Ile Thr Gln Trp Thr Arg Thr Pro Gln Asn Gln Ser
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Glu Val Glu Ile Ala
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<222> (93)..(113)

<223> Putative membrane-spanning segment

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0996264.09260

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<223> Certain membrane-spanning segment

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<222> (209)..(229)

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<223> Putative membrane-spanning segment

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Ala Lys Val Glu Lys Met Tyr Pro Ile Met Glu Tyr Ser Cys Ser Asp
20 25 30

Arg Asn Leu Val Leu Ile Tyr Gly Ile Leu Leu Ile Tyr Ile Tyr Ile
35 40 45

Gly Asn Leu Asn Val Ala Arg His Phe Ser Met Lys Thr Pro Val Ala
50 55 60

Arg Ser Asn Ile Lys Leu Ile Leu Thr Asn Asn Val Lys Trp Leu His
65 70 75 80

Lys Lys Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu
85 90 95

Leu Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu Met
100 105 110

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09966264-092804

Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu Arg Cys Tyr Leu Ser
115 120 125

Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu Cys Phe Pro Gly His
130 135 140

Asn Val Gly Ser Leu Phe His Met Ala Asp Asp Leu Gly Arg Ala Met
145 150 155 160

Glu Ser Leu Val Ser Val Met Thr Asp Glu Glu Gly Ala Glu Lys Met
165 170 175

Phe Tyr Asn Ser Arg Phe Pro His Gly Phe Tyr Asn Ile His Thr Thr
180 185 190

Lys Arg Ile Arg Gln Lys Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu
195 200 205

Arg Arg Val Val Val Leu Tyr Cys Arg Phe Gln Lys Phe Leu Ser Leu
210 215 220

Leu Leu Phe Cys Lys Gln Trp Gln Val Leu His Val Tyr Ala Ile Val
225 230 235 240

Gln Lys Ser Tyr Lys Lys Thr Thr Cys Lys Ile Leu Ile Ala Lys Lys
245 250 255

Leu Ala Ile Ser Leu Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu
260 265 270

Lys Gln Leu Lys Arg Lys Asn Tyr Lys Gly Lys Arg Lys Lys Arg Asn
275 280 285

Gly Gln Val Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn
290 295 300

Thr Pro Lys Pro Lys Arg Gly Arg Asn Ser Met Arg Ser Arg Val Arg
305 310 315 320

Cys Lys Leu Ile

0996264-09301

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<211> 15

<212> DNA

<213> human

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<211> 234

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Phe Pro Ile Gln Cys Ile Val His Gln Arg Ser Ile Gln Glu Phe Ile
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att att att ttc aac cca agt aaa agc aga gag aaa ata gcc acc tcc 96
Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala Thr Ser
20 25 30

acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg aaa tga 144
Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu Lys
35 40 45

aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc gat ggt 192
Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp Gly
50 55 60

tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg 234
Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met
65 70 75